



Blast 2 Sequences results

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Taxonomy

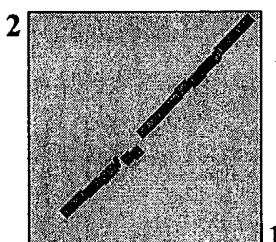
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** gap open:**11** gap extension:**1**
 x_dropoff: **50** expect:**10.000** wordsize: **3** Filter Align

Sequence 1 gi_1362047 cysteine proteinase (EC 3.4.22.-) precursor - soybean **Length 380 (1 .. 380)**

Sequence 2 lcl|seq_2 **Length 366 (1 .. 366)**



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 204 bits (520), Expect = 4e-51
 Identities = 133/336 (39%), Positives = 181/336 (53%), Gaps = 67/336 (19%)

Query: 59 ENYGRSystEEEYLRLGIFAQNMRRAEHQALDPTAVHGVTQFSDLTEDEFEKLYTGVN 118
 E++ ++ T+ R IF + + EH+A H T+FSDLT + +L
 Sbjct: 56 EDHHLAFKTKFAKDHRFRIFKHHFSQE-EHRAKS---HQKTRFSDLTGLKPLRLLD--- 107

Query: 119 GGFPSSNNAAAGG--IAPPLEVDGLPE---NFDWREKGAVTEVKLQGRGSCWAFSTTGSI 173
 PS+ + G + P+ G + +FDW QG CG CW+
 Sbjct: 108 ---PSAPSEFRGQFLKAPIRDHGPSDAQTDFDW-----QGSCGWCS----- 146

Query: 174 EGANFLATGK-----LVSLSEQQLLDCKDNKCITEKTSCDNGCN 212
 EGA+FL+TG LVSLSEQQL+DCD++CD E+ +CD+GCN
 Sbjct: 147 EGAHFLSTGLPTSDLPAVTGVKNFSAVGALGLVSLSEQQLVDCDHECDPEERGACDSGCN 206

Query: 213 GGLMTNAYNYXXXXXXXXXXXXXXPYTGERGECKF-DPEKIAVKITNFTNIPADENQIAAY 271
 GGLMT A+ Y YPYTG + K P KIA + NF+ + QIAA
 Sbjct: 207 GGLMTTAFETYTLKAGGLMREEDYPYTGRFDKSKDRGPCKIAASVANFSVV----QIAAN 261

Query: 272 LVKNGPLAMGVNAIFMQTYIGGVSCPLICSKKRLNHGVL----LVGYAKGFSILRLGN 326
 LVKNGP A+ + ++ + +G VSCP IC K L+HGVL LVGYG+ ++ +R
 Sbjct: 262 LVKNGPNAVMQSLDEELAVGIVSCPYICGK-HLDHGVLTYIGGLVGYGSGAYAPIRFKE 320

Query: 327 KPYWIICKNSWGEKWGEDGYYKLCRGHGMCGINTMVS 362
 KPYWIICKNSWGE WGE+GYYK+CRG +CG+++MVS
 Sbjct: 321 KPYWIICKNSWGESWGEEGYYYKICRGRNVCGVDSMVS 356

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda	K	H
0.318	0.136	0.416

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 1122
Number of Sequences: 0
Number of extensions: 96
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 380
length of database: 741,981,269
effective HSP length: 132
effective length of query: 248
effective length of database: 741,981,137
effective search space: 184011321976
effective search space used: 184011321976
T: 9
A: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 77 (34.3 bits)